

SEQUENCE LISTING

<110> Jenuwein, Thomas
Laible, Gotz
O'Carroll, Donal
Eisenhaber, Frank
Rea, Stephen

<120> Chromatin-Regulator Genes

<130> 0652.1670001

<140> US 09/589,892

<141> 2000-06-09

<150> US 08/945,988

<151> 1997-11-10

<150> PCT/EP96/01818

<151> 1996-05-02

<150> DE 195 16 776.7

<151> 1995-05-10

<160> 21

<170> PatentIn version 3.2

<210> 1

<211> 2600

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)..(89)

<220>

<221> CDS

<222> (90)..(2330)

<220>

<221> 3'UTR

<222> (2331)..(2600)

<400> 1

aggcagtgga gccccggcgg cggcggcggc ggcgcgcggg ggcgacgcgc gggaacaacg 60

cgagtcggcg cgcgggacga agaataatc atg ggc cag act ggg aag aaa tct 113
Met Gly Gln Thr Gly Lys Lys Ser
1 5

gag aag gga cca gtt tgt tgg cgg aag cgt gta aaa tca gag tac atg 161
Glu Lys Gly Pro Val Cys Trp Arg Lys Arg Val Lys Ser Glu Tyr Met
10 15 20

cga ctg aga cag ctc aag agg ttc aga cga gct gat gaa gta aag agt 209
Arg Leu Arg Gln Leu Lys Arg Phe Arg Arg Ala Asp Glu Val Lys Ser
25 30 35 40

atg ttt agt tcc aat cgt cag aaa att ttg gaa aga acg gaa atc tta 257

Met	Phe	Ser	Ser	Asn	Arg	Gln	Lys	Ile	Leu	Glu	Arg	Thr	Glu	Ile	Leu		
				45					50					55			
aac	caa	gaa	tgg	aaa	cag	cga	agg	ata	cag	cct	gtg	cac	atc	ctg	act	305	
Asn	Gln	Glu	Trp	Lys	Gln	Arg	Arg	Ile	Gln	Pro	Val	His	Ile	Leu	Thr		
			60					65					70				
tct	gtg	agc	tca	ttg	cgc	ggg	act	agg	gag	tgt	tcg	gtg	acc	agt	gac	353	
Ser	Val	Ser	Ser	Leu	Arg	Gly	Thr	Arg	Glu	Cys	Ser	Val	Thr	Ser	Asp		
		75					80					85					
ttg	gat	ttt	cca	aca	caa	gtc	atc	cca	tta	aag	act	ctg	aat	gca	gtt	401	
Leu	Asp	Phe	Pro	Thr	Gln	Val	Ile	Pro	Leu	Lys	Thr	Leu	Asn	Ala	Val		
	90					95					100						
gct	tca	gta	ccc	ata	atg	tat	tct	tgg	tct	ccc	cta	cag	cag	aat	ttt	449	
Ala	Ser	Val	Pro	Ile	Met	Tyr	Ser	Trp	Ser	Pro	Leu	Gln	Gln	Asn	Phe		
105					110					115					120		
atg	gtg	gaa	gat	gaa	act	gtt	tta	cat	aac	att	cct	tat	atg	gga	gat	497	
Met	Val	Glu	Asp	Glu	Thr	Val	Leu	His	Asn	Ile	Pro	Tyr	Met	Gly	Asp		
				125					130					135			
gaa	gtt	tta	gat	cag	gat	ggg	act	ttc	att	gaa	gaa	cta	ata	aaa	aat	545	
Glu	Val	Leu	Asp	Gln	Asp	Gly	Thr	Phe	Ile	Glu	Glu	Leu	Ile	Lys	Asn		
			140					145					150				
tat	gat	ggg	aaa	gta	cac	ggg	gat	aga	gaa	tgt	ggg	ttt	ata	aat	gat	593	
Tyr	Asp	Gly	Lys	Val	His	Gly	Asp	Arg	Glu	Cys	Gly	Phe	Ile	Asn	Asp		
		155					160					165					
gaa	att	ttt	gtg	gag	ttg	gtg	aat	gcc	ctt	ggg	caa	tat	aat	gat	gat	641	
Glu	Ile	Phe	Val	Glu	Leu	Val	Asn	Ala	Leu	Gly	Gln	Tyr	Asn	Asp	Asp		
	170					175					180						
gac	gat	gat	gat	gat	gga	gac	gat	cct	gaa	gaa	aga	gaa	gaa	aag	cag	689	
Asp	Asp	Asp	Asp	Asp	Gly	Asp	Asp	Pro	Glu	Glu	Arg	Glu	Glu	Lys	Gln		
185					190					195					200		
aaa	gat	ctg	gag	gat	cac	cga	gat	gat	aaa	gaa	agc	cgc	cca	cct	cgg	737	
Lys	Asp	Leu	Glu	Asp	His	Arg	Asp	Asp	Lys	Glu	Ser	Arg	Pro	Pro	Arg		
			205						210					215			
aaa	ttt	cct	tct	gat	aaa	att	ttt	gaa	gcc	att	tcc	tca	atg	ttt	cca	785	
Lys	Phe	Pro	Ser	Asp	Lys	Ile	Phe	Glu	Ala	Ile	Ser	Ser	Met	Phe	Pro		
			220					225					230				
gat	aag	ggc	aca	gca	gaa	gaa	cta	aag	gaa	aaa	tat	aaa	gaa	ctc	acc	833	
Asp	Lys	Gly	Thr	Ala	Glu	Glu	Leu	Lys	Glu	Lys	Tyr	Lys	Glu	Leu	Thr		
		235					240					245					
gaa	cag	cag	ctc	cca	ggc	gca	ctt	cct	cct	gaa	tgt	acc	ccc	aac	ata	881	
Glu	Gln	Gln	Leu	Pro	Gly	Ala	Leu	Pro	Pro	Glu	Cys	Thr	Pro	Asn	Ile		
	250					255					260						
gat	gga	cca	aat	gct	aaa	tct	gtt	cag	aga	gag	caa	agc	tta	cac	tcc	929	
Asp	Gly	Pro	Asn	Ala	Lys	Ser	Val	Gln	Arg	Glu	Gln	Ser	Leu	His	Ser		
	265				270					275					280		
ttt	cat	acg	ctt	ttc	tgt	agg	cga	tgt	ttt	aaa	tat	gac	tgc	ttc	cta	977	
Phe	His	Thr	Leu	Phe	Cys	Arg	Arg	Cys	Phe	Lys	Tyr	Asp	Cys	Phe	Leu		
			285					290						295			

cat cct ttt cat gca aca ccc aac act tat aag cgg aag aac aca gaa	1025
His Pro Phe His Ala Thr Pro Asn Thr Tyr Lys Arg Lys Asn Thr Glu	
300 305 310	
aca gct cta gac aac aaa cct tgt gga cca cag tgt tac cag cat ttg	1073
Thr Ala Leu Asp Asn Lys Pro Cys Gly Pro Gln Cys Tyr Gln His Leu	
315 320 325	
gag gga gca aag gag ttt gct gct gct ctc acc gct gag cgg ata aag	1121
Glu Gly Ala Lys Glu Phe Ala Ala Ala Leu Thr Ala Glu Arg Ile Lys	
330 335 340	
acc cca cca aaa cgt cca gga ggc cgc aga aga gga cgg ctt ccc aat	1169
Thr Pro Pro Lys Arg Pro Gly Gly Arg Arg Arg Gly Arg Leu Pro Asn	
345 350 355 360	
aac agt agc agg ccc agc acc ccc acc att aat gtg ctg gaa tca aag	1217
Asn Ser Ser Arg Pro Ser Thr Pro Thr Ile Asn Val Leu Glu Ser Lys	
365 370 375	
gat aca gac agt gat agg gaa gca ggg act gaa acg ggg gga gag aac	1265
Asp Thr Asp Ser Asp Arg Glu Ala Gly Thr Glu Thr Gly Gly Glu Asn	
380 385 390	
aat gat aaa gaa gaa gaa gag aag aaa gat gaa act tcg agc tcc tct	1313
Asn Asp Lys Glu Glu Glu Glu Lys Lys Asp Glu Thr Ser Ser Ser Ser	
395 400 405	
gaa gca aat tct cgg tgt caa aca cca ata aag atg aag cca aat att	1361
Glu Ala Asn Ser Arg Cys Gln Thr Pro Ile Lys Met Lys Pro Asn Ile	
410 415 420	
gaa cct cct gag aat gtg gag tgg agt ggt gct gaa gcc tca atg ttt	1409
Glu Pro Pro Glu Asn Val Glu Trp Ser Gly Ala Glu Ala Ser Met Phe	
425 430 435 440	
aga gtc ctc att ggc act tac tat gac aat ttc tgt gcc att gct agg	1457
Arg Val Leu Ile Gly Thr Tyr Tyr Asp Asn Phe Cys Ala Ile Ala Arg	
445 450 455	
tta att ggg acc aaa aca tgt aga cag gtg tat gag ttt aga gtc aaa	1505
Leu Ile Gly Thr Lys Thr Cys Arg Gln Val Tyr Glu Phe Arg Val Lys	
460 465 470	
gaa tct agc atc ata gct cca gct ccc gct gag gat gtg gat act cct	1553
Glu Ser Ser Ile Ile Ala Pro Ala Pro Ala Glu Asp Val Asp Thr Pro	
475 480 485	
cca agg aaa aag aag agg aaa cac cgg ttg tgg gct gca cac tgc aga	1601
Pro Arg Lys Lys Lys Arg Lys His Arg Leu Trp Ala Ala His Cys Arg	
490 495 500	
aag ata cag ctg aaa aag gac ggc tcc tct aac cat gtt tac aac tat	1649
Lys Ile Gln Leu Lys Lys Asp Gly Ser Ser Asn His Val Tyr Asn Tyr	
505 510 515 520	
caa ccc tgt gat cat cca cgg cag cct tgt gac agt tcg tgc cct tgt	1697
Gln Pro Cys Asp His Pro Arg Gln Pro Cys Asp Ser Ser Cys Pro Cys	
525 530 535	
gtg ata gca caa aat ttt tgt gaa aag ttt tgt caa tgt agt tca gag	1745
Val Ile Ala Gln Asn Phe Cys Glu Lys Phe Cys Gln Cys Ser Ser Glu	

540	545	550	
tgt caa aac cgc ttt ccg gga tgc cgc tgc aaa gca cag tgc aac acc Cys Gln Asn Arg Phe Pro Gly Cys Arg Cys Lys Ala Gln Cys Asn Thr 555 560 565			1793
aag cag tgc ccg tgc tac ctg gct gtc cga gag tgt gac cct gac ctc Lys Gln Cys Pro Cys Tyr Leu Ala Val Arg Glu Cys Asp Pro Asp Leu 570 575 580			1841
tgt ctt act tgt gga gcc gct gac cat tgg gac agt aaa aat gtg tcc Cys Leu Thr Cys Gly Ala Ala Asp His Trp Asp Ser Lys Asn Val Ser 585 590 595 600			1889
tgc aag aac tgc agt att cag cgg ggc tcc aaa aag cat cta ttg ctg Cys Lys Asn Cys Ser Ile Gln Arg Gly Ser Lys Lys His Leu Leu Leu 605 610 615			1937
gca cca tct gac gtg gca ggc tgg ggg att ttt atc aaa gat cct gtg Ala Pro Ser Asp Val Ala Gly Trp Gly Ile Phe Ile Lys Asp Pro Val 620 625 630			1985
cag aaa aat gaa ttc atc tca gaa tac tgt gga gag att att tct caa Gln Lys Asn Glu Phe Ile Ser Glu Tyr Cys Gly Glu Ile Ile Ser Gln 635 640 645			2033
gat gaa gct gac aga aga ggg aaa gtg tat gat aaa tac atg tgc agc Asp Glu Ala Asp Arg Arg Gly Lys Val Tyr Asp Lys Tyr Met Cys Ser 650 655 660			2081
ttt ctg ttc aac ttg aac aat gat ttt gtg gtg gat gca acc cgc aag Phe Leu Phe Asn Leu Asn Asn Asp Phe Val Val Asp Ala Thr Arg Lys 665 670 675 680			2129
ggt aac aaa att cgt ttt gca aat cat tcg gta aat cca aac tgc tat Gly Asn Lys Ile Arg Phe Ala Asn His Ser Val Asn Pro Asn Cys Tyr 685 690 695			2177
gca aaa gtt atg atg gtt aac ggt gat cac agg ata ggt att ttt gcc Ala Lys Val Met Met Val Asn Gly Asp His Arg Ile Gly Ile Phe Ala 700 705 710			2225
aag aga gcc atc cag act ggc gaa gag ctg ttt ttt gat tac aga tac Lys Arg Ala Ile Gln Thr Gly Glu Leu Phe Phe Asp Tyr Arg Tyr 715 720 725			2273
agc cag gct gat gcc ctg aag tat gtc ggc atc gaa aga gaa atg gaa Ser Gln Ala Asp Ala Leu Lys Tyr Val Gly Ile Glu Arg Glu Met Glu 730 735 740			2321
atc cct tga catctgctac ctctctcccc tcctctgaaa cagctgcctt Ile Pro 745			2370
agcttcagga acctcgagta ctgtgggcaa tttagaaaaa gaacatgcag tttgaaattc			2430
tgaatttgca aagtactgta agaataattt atagtaatga gtttaaaaaat caacttttta			2490
ttgcctttctc accagctgca aagtgttttg taccagtga tttttgcaat aatgcagtat			2550
ggtacatttt tcaactttga ataaagaata cttgaacttg tcaaaaaaaaa			2600

<210> 2
 <211> 746
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Gly Gln Thr Gly Lys Lys Ser Glu Lys Gly Pro Val Cys Trp Arg
 1 5 10 15

Lys Arg Val Lys Ser Glu Tyr Met Arg Leu Arg Gln Leu Lys Arg Phe
 20 25 30

Arg Arg Ala Asp Glu Val Lys Ser Met Phe Ser Ser Asn Arg Gln Lys
 35 40 45

Ile Leu Glu Arg Thr Glu Ile Leu Asn Gln Glu Trp Lys Gln Arg Arg
 50 55 60

Ile Gln Pro Val His Ile Leu Thr Ser Val Ser Ser Leu Arg Gly Thr
 65 70 75 80

Arg Glu Cys Ser Val Thr Ser Asp Leu Asp Phe Pro Thr Gln Val Ile
 85 90 95

Pro Leu Lys Thr Leu Asn Ala Val Ala Ser Val Pro Ile Met Tyr Ser
 100 105 110

Trp Ser Pro Leu Gln Gln Asn Phe Met Val Glu Asp Glu Thr Val Leu
 115 120 125

His Asn Ile Pro Tyr Met Gly Asp Glu Val Leu Asp Gln Asp Gly Thr
 130 135 140

Phe Ile Glu Glu Leu Ile Lys Asn Tyr Asp Gly Lys Val His Gly Asp
 145 150 155 160

Arg Glu Cys Gly Phe Ile Asn Asp Glu Ile Phe Val Glu Leu Val Asn
 165 170 175

Ala Leu Gly Gln Tyr Asn Asp Asp Asp Asp Asp Asp Gly Asp Asp
 180 185 190

Pro Glu Glu Arg Glu Glu Lys Gln Lys Asp Leu Glu Asp His Arg Asp
 195 200 205

Asp Lys Glu Ser Arg Pro Pro Arg Lys Phe Pro Ser Asp Lys Ile Phe
 210 215 220

Glu Ala Ile Ser Ser Met Phe Pro Asp Lys Gly Thr Ala Glu Glu Leu
225 230 235 240

Lys Glu Lys Tyr Lys Glu Leu Thr Glu Gln Gln Leu Pro Gly Ala Leu
245 250 255

Pro Pro Glu Cys Thr Pro Asn Ile Asp Gly Pro Asn Ala Lys Ser Val
260 265 270

Gln Arg Glu Gln Ser Leu His Ser Phe His Thr Leu Phe Cys Arg Arg
275 280 285

Cys Phe Lys Tyr Asp Cys Phe Leu His Pro Phe His Ala Thr Pro Asn
290 295 300

Thr Tyr Lys Arg Lys Asn Thr Glu Thr Ala Leu Asp Asn Lys Pro Cys
305 310 315 320

Gly Pro Gln Cys Tyr Gln His Leu Glu Gly Ala Lys Glu Phe Ala Ala
325 330 335

Ala Leu Thr Ala Glu Arg Ile Lys Thr Pro Pro Lys Arg Pro Gly Gly
340 345 350

Arg Arg Arg Gly Arg Leu Pro Asn Asn Ser Ser Arg Pro Ser Thr Pro
355 360 365

Thr Ile Asn Val Leu Glu Ser Lys Asp Thr Asp Ser Asp Arg Glu Ala
370 375 380

Gly Thr Glu Thr Gly Gly Glu Asn Asn Asp Lys Glu Glu Glu Glu Lys
385 390 395 400

Lys Asp Glu Thr Ser Ser Ser Ser Glu Ala Asn Ser Arg Cys Gln Thr
405 410 415

Pro Ile Lys Met Lys Pro Asn Ile Glu Pro Pro Glu Asn Val Glu Trp
420 425 430

Ser Gly Ala Glu Ala Ser Met Phe Arg Val Leu Ile Gly Thr Tyr Tyr
435 440 445

Asp Asn Phe Cys Ala Ile Ala Arg Leu Ile Gly Thr Lys Thr Cys Arg
450 455 460

Gln Val Tyr Glu Phe Arg Val Lys Glu Ser Ser Ile Ile Ala Pro Ala
465 470 475 480

Pro Ala Glu Asp Val Asp Thr Pro Pro Arg Lys Lys Lys Arg Lys His
485 490 495

Arg Leu Trp Ala Ala His Cys Arg Lys Ile Gln Leu Lys Lys Asp Gly
500 505 510

Ser Ser Asn His Val Tyr Asn Tyr Gln Pro Cys Asp His Pro Arg Gln
515 520 525

Pro Cys Asp Ser Ser Cys Pro Cys Val Ile Ala Gln Asn Phe Cys Glu
530 535 540

Lys Phe Cys Gln Cys Ser Ser Glu Cys Gln Asn Arg Phe Pro Gly Cys
545 550 555 560

Arg Cys Lys Ala Gln Cys Asn Thr Lys Gln Cys Pro Cys Tyr Leu Ala
565 570 575

Val Arg Glu Cys Asp Pro Asp Leu Cys Leu Thr Cys Gly Ala Ala Asp
580 585 590

His Trp Asp Ser Lys Asn Val Ser Cys Lys Asn Cys Ser Ile Gln Arg
595 600 605

Gly Ser Lys Lys His Leu Leu Leu Ala Pro Ser Asp Val Ala Gly Trp
610 615 620

Gly Ile Phe Ile Lys Asp Pro Val Gln Lys Asn Glu Phe Ile Ser Glu
625 630 635 640

Tyr Cys Gly Glu Ile Ile Ser Gln Asp Glu Ala Asp Arg Arg Gly Lys
645 650 655

Val Tyr Asp Lys Tyr Met Cys Ser Phe Leu Phe Asn Leu Asn Asn Asp
660 665 670

Phe Val Val Asp Ala Thr Arg Lys Gly Asn Lys Ile Arg Phe Ala Asn
675 680 685

His Ser Val Asn Pro Asn Cys Tyr Ala Lys Val Met Met Val Asn Gly
690 695 700

Asp His Arg Ile Gly Ile Phe Ala Lys Arg Ala Ile Gln Thr Gly Glu
705 710 715 720

Glu Leu Phe Phe Asp Tyr Arg Tyr Ser Gln Ala Asp Ala Leu Lys Tyr

725

730

735

Val Gly Ile Glu Arg Glu Met Glu Ile Pro
740 745

<210> 3
<211> 2732
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> (1)..(44)

<220>
<221> CDS
<222> (45)..(1283)

<220>
<221> 3'UTR
<222> (1284)..(2732)

<400> 3
tcgcgaggcc ggctaggccc gaatgtcggt agccgtgggg aaag atg gcg gaa aat 56
Met Ala Glu Asn
1

tta aaa ggc tgc agc gtg tgt tgc aag tct tct tgg aat cag ctg cag 104
Leu Lys Gly Cys Ser Val Cys Cys Lys Ser Ser Trp Asn Gln Leu Gln
5 10 15 20

gac ctg tgc cgc ctg gcc aag ctc tcc tgc cct gcc ctc ggt atc tct 152
Asp Leu Cys Arg Leu Ala Lys Leu Ser Cys Pro Ala Leu Gly Ile Ser
25 30 35

aag agg aac ctc tat gac ttt gaa gtc gag tac ctg tgc gat tac aag 200
Lys Arg Asn Leu Tyr Asp Phe Glu Val Glu Tyr Leu Cys Asp Tyr Lys
40 45 50

aag atc cgc gaa cag gaa tat tac ctg gtg aaa tgg cgt gga tat cca 248
Lys Ile Arg Glu Gln Glu Tyr Tyr Leu Val Lys Trp Arg Gly Tyr Pro
55 60 65

gac tca gag agc acc tgg gag cca cgg cag aat ctc aag tgt gtg cgt 296
Asp Ser Glu Ser Thr Trp Glu Pro Arg Gln Asn Leu Lys Cys Val Arg
70 75 80

atc ctc aag cag ttc cac aag gac tta gaa agg gag ctg ctc cgg cgg 344
Ile Leu Lys Gln Phe His Lys Asp Leu Glu Arg Glu Leu Leu Arg Arg
85 90 95 100

cac cac cgg tca aag acc ccc cgg cac ctg gag cca agc ttg gcc aac 392
His His Arg Ser Lys Thr Pro Arg His Leu Asp Pro Ser Leu Ala Asn
105 110 115

tac ctg gtg cag aag gcc aag cag agg cgg gcg ctc cgt cgc tgg gag 440
Tyr Leu Val Gln Lys Ala Lys Gln Arg Arg Ala Leu Arg Arg Trp Glu
120 125 130

cag gag ctc aat gcc aag cgc agc cat ctg gga cgc atc act gta gag	488
Gln Glu Leu Asn Ala Lys Arg Ser His Leu Gly Arg Ile Thr Val Glu	
135 140 145	
aat gag gtg gac ctg gac ggc cct ccg cgg gcc ttc gtg tac atc aat	536
Asn Glu Val Asp Leu Asp Gly Pro Pro Arg Ala Phe Val Tyr Ile Asn	
150 155 160	
gag tac cgt gtt ggt gag ggc atc acc ctc aac cag gtg gct gtg ggc	584
Glu Tyr Arg Val Gly Glu Gly Ile Thr Leu Asn Gln Val Ala Val Gly	
165 170 175 180	
tgc gag tgc cag gac tgt ctg tgg gca ccc act gga ggc tgc tgc ccg	632
Cys Glu Cys Gln Asp Cys Leu Trp Ala Pro Thr Gly Gly Cys Cys Pro	
185 190 195	
ggg gcg tca ctg cac aag ttt gcc tac aat gac cag ggc cag gtg cgg	680
Gly Ala Ser Leu His Lys Phe Ala Tyr Asn Asp Gln Gly Gln Val Arg	
200 205 210	
ctt cga gcc ggg ctg ccc atc tac gag tgc aac tcc cgc tgc cgc tgc	728
Leu Arg Ala Gly Leu Pro Ile Tyr Glu Cys Asn Ser Arg Cys Arg Cys	
215 220 225	
ggc tat gac tgc cca aat cgt gtg gta cag aag ggt atc cga tat gac	776
Gly Tyr Asp Cys Pro Asn Arg Val Val Gln Lys Gly Ile Arg Tyr Asp	
230 235 240	
ctc tgc atc ttc cgg acg gat gat ggg cgt ggc tgg ggc gtc cgc acc	824
Leu Cys Ile Phe Arg Thr Asp Asp Gly Arg Gly Trp Gly Val Arg Thr	
245 250 255 260	
ctg gag aag att cgc aag aac agc ttc gtc atg gag tac gtg gga gag	872
Leu Glu Lys Ile Arg Lys Asn Ser Phe Val Met Glu Tyr Val Gly Glu	
265 270 275	
atc att acc tca gag gag gca gag cgg cgg ggc cag atc tac gac cgt	920
Ile Ile Thr Ser Glu Glu Ala Glu Arg Arg Gly Gln Ile Tyr Asp Arg	
280 285 290	
cag ggc gcc acc tac ctc ttt gac ctg gac tac gtg gag gac gtg tac	968
Gln Gly Ala Thr Tyr Leu Phe Asp Leu Asp Tyr Val Glu Asp Val Tyr	
295 300 305	
acc gtg gat gcc gcc tac tat ggc aac atc tcc cac ttt gtc aac cac	1016
Thr Val Asp Ala Ala Tyr Tyr Gly Asn Ile Ser His Phe Val Asn His	
310 315 320	
agt tgt gac ccc aac ctg cag gtg tac aac gtc ttc ata gac aac ctt	1064
Ser Cys Asp Pro Asn Leu Gln Val Tyr Asn Val Phe Ile Asp Asn Leu	
325 330 335 340	
gac gag cgg ctg ccc cgc atc gct ttc ttt gcc aca aga acc atc cgg	1112
Asp Glu Arg Leu Pro Arg Ile Ala Phe Phe Ala Thr Arg Thr Ile Arg	
345 350 355	
gca ggc gag gag ctc acc ttt gat tac aac atg caa gtg gac ccc gtg	1160
Ala Gly Glu Glu Leu Thr Phe Asp Tyr Asn Met Gln Val Asp Pro Val	
360 365 370	
gac atg gag agc acc cgc atg gac tcc aac ttt ggc ctg gct ggg ctc	1208
Asp Met Glu Ser Thr Arg Met Asp Ser Asn Phe Gly Leu Ala Gly Leu	

375	380	385	
cct ggc tcc cct aag aag cgg gtc cgt att gaa tgc aag tgt ggg act			1256
Pro Gly Ser Pro Lys Lys Arg Val Arg Ile Glu Cys Lys Cys Gly Thr			
390	395	400	
gag tcc tgc cgc aaa tac ctc ttc tag cccttagaag tctgaggcca			1303
Glu Ser Cys Arg Lys Tyr Leu Phe			
405	410		
gactgactga gggggcctga agctacatgc acctccccca ctgctgccct cctgtcgaga			1363
atgactgccca gggcctcgcc tgccctccacc tgccccacc tgctcctacc tgctctacgt			1423
tcagggtgtg ggccgtggtg aggaccgact ccaggagtcc cctttccctg tcccagcccc			1483
atctgtgggt tgcacttaca aacccccacc caccttcaga aatagttttt caacatcaag			1543
actctctgtc gttgggattc atggcctatt aaggaggtcc aagggggtgag tcccaaccca			1603
gccccagaat atatttgttt ttgcacctgc ttctgcctgg agattgaggg gtctgtctgca			1663
ggcctcctcc ctgctgcccc aaaggtatgg ggaagcaacc ccagagcagg cagacatcag			1723
aggccagagt gcctagcccc acatgaagct ggttccccaa ccacagaaac tttgtactag			1783
tgaaagaaag gggtcctctg cctacgggct gaggtgtggt tctgtctctg cttacagtgc			1843
tgggtagtgt tggccctaag agctgtaggg tctcttcttc agggctgcat atctgagaag			1903
tggatgcca catgccactg gaagggaagt ggggtgtccat gggccactga gcagtgagag			1963
gaaggcagtg cagagctggc cagccctgga ggtaggctgg gaccaagctc tgcttcaca			2023
gtgcagtga ggtacctagg gctcttggga gctctgcggt tgctaggggc cctgacctgg			2083
ggtgtcatga ccgctgacac cactcagagc tggaaccaag atctagatag tccgtagata			2143
gcacttagga caagaatgtg cattgatggg gtgggtgatga ggtgccaggc actaggtaga			2203
gcacctggtc cacgtggatt gtctcagga agccttgaaa accacggagg tggatgccag			2263
gaaagggccc atgtggcaga aggcaaagta caggccaaga attgggggtg ggggagatgg			2323
cttccccact atgggatgac gaggcgagag ggaagccctt gctgcctgcc attcccagac			2383
cccagccctt tgtgtctacc ctgggtccac tgggtctcaa agtcacctgc ctacaaatgt			2443
acaaaaggcg aaggttctga tggtgcctt gctccttgct cccccacccc ctgtgaggac			2503
ttctctagga agtccttcct gactacctgt gccagagtg cccctacatg agactgtatg			2563
ccctgctatc agatgccaga tctatgtgtc tgtctgtgtg tccatcccgc cggccccca			2623
gactaacctc caggcatgga ctgaatctgg ttctcctctt gtacaccctt caaccctatg			2683
cagcctggag tgggcatcaa taaaatgaac tgtcgactga aaaaaaaaa			2732

<210> 4
 <211> 412
 <212> PRT

<213> Homo sapiens

<400> 4

Met Ala Glu Asn Leu Lys Gly Cys Ser Val Cys Cys Lys Ser Ser Trp
1 5 10 15

Asn Gln Leu Gln Asp Leu Cys Arg Leu Ala Lys Leu Ser Cys Pro Ala
20 25 30

Leu Gly Ile Ser Lys Arg Asn Leu Tyr Asp Phe Glu Val Glu Tyr Leu
35 40 45

Cys Asp Tyr Lys Lys Ile Arg Glu Gln Glu Tyr Tyr Leu Val Lys Trp
50 55 60

Arg Gly Tyr Pro Asp Ser Glu Ser Thr Trp Glu Pro Arg Gln Asn Leu
65 70 75 80

Lys Cys Val Arg Ile Leu Lys Gln Phe His Lys Asp Leu Glu Arg Glu
85 90 95

Leu Leu Arg Arg His His Arg Ser Lys Thr Pro Arg His Leu Asp Pro
100 105 110

Ser Leu Ala Asn Tyr Leu Val Gln Lys Ala Lys Gln Arg Arg Ala Leu
115 120 125

Arg Arg Trp Glu Gln Glu Leu Asn Ala Lys Arg Ser His Leu Gly Arg
130 135 140

Ile Thr Val Glu Asn Glu Val Asp Leu Asp Gly Pro Pro Arg Ala Phe
145 150 155 160

Val Tyr Ile Asn Glu Tyr Arg Val Gly Glu Gly Ile Thr Leu Asn Gln
165 170 175

Val Ala Val Gly Cys Glu Cys Gln Asp Cys Leu Trp Ala Pro Thr Gly
180 185 190

Gly Cys Cys Pro Gly Ala Ser Leu His Lys Phe Ala Tyr Asn Asp Gln
195 200 205

Gly Gln Val Arg Leu Arg Ala Gly Leu Pro Ile Tyr Glu Cys Asn Ser
210 215 220

Arg Cys Arg Cys Gly Tyr Asp Cys Pro Asn Arg Val Val Gln Lys Gly
225 230 235 240

Ile Arg Tyr Asp Leu Cys Ile Phe Arg Thr Asp Asp Gly Arg Gly Trp
245 250 255

Gly Val Arg Thr Leu Glu Lys Ile Arg Lys Asn Ser Phe Val Met Glu
260 265 270

Tyr Val Gly Glu Ile Ile Thr Ser Glu Glu Ala Glu Arg Arg Gly Gln
275 280 285

Ile Tyr Asp Arg Gln Gly Ala Thr Tyr Leu Phe Asp Leu Asp Tyr Val
290 295 300

Glu Asp Val Tyr Thr Val Asp Ala Ala Tyr Tyr Gly Asn Ile Ser His
305 310 315 320

Phe Val Asn His Ser Cys Asp Pro Asn Leu Gln Val Tyr Asn Val Phe
325 330 335

Ile Asp Asn Leu Asp Glu Arg Leu Pro Arg Ile Ala Phe Phe Ala Thr
340 345 350

Arg Thr Ile Arg Ala Gly Glu Glu Leu Thr Phe Asp Tyr Asn Met Gln
355 360 365

Val Asp Pro Val Asp Met Glu Ser Thr Arg Met Asp Ser Asn Phe Gly
370 375 380

Leu Ala Gly Leu Pro Gly Ser Pro Lys Lys Arg Val Arg Ile Glu Cys
385 390 395 400

Lys Cys Gly Thr Glu Ser Cys Arg Lys Tyr Leu Phe
405 410

<210> 5

<211> 489

<212> DNA

<213> Homo sapiens

<400> 5

actcacctgt ggggcctcag agcactggga ctgcaagggtg gtttcctgta aaaactgcag 60

catccagcgt ggacttaaga agcacctgct gctggccccc tctgatgtgg ccggatgggg 120

caccttcata aaggagtctg tgcagaagaa cgaattcatt tctgaatact gtggtgagct 180

catctctcag gatgaggctg atcgacgcgg aaaggtctat gacaaataca tgtccagctt 240

cctcttcaac ctcaataatg atttttagt ggatgctact cggaaggaa acaaaattcg 300

atttgcaaat cattcagtga atcccaactg ttatgccaaa ggtgagtccc agtaacctgg 360

gaggtgggggt gggggatgga tgcctcttta ctgtgatttc cattcgttgt tgaacatttt 420
 ccttagctga gctatctttt gtccaaagat aatcatgatt aatatctggt atcatttttag 480
 gccctcttc 489

<210> 6
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> EcoRI Adaptor oligonucleotide

<400> 6
 aattctcgag ctgctcgaca 20

<210> 7
 <211> 31
 <212> DNA
 <213> Drosophila melanogaster

<400> 7
 actgaattcg gctggggcat ctttcttaag g 31

<210> 8
 <211> 31
 <212> DNA
 <213> Drosophila melanogaster

<400> 8
 actctagaca atttccattt cacgctctat g 31

<210> 9
 <211> 30
 <212> DNA
 <213> Drosophila melanogaster.

<400> 9
 atatagtact tcaagtccat tcaaaagagg 30

<210> 10
 <211> 29
 <212> DNA
 <213> Drosophila melanogaster

<400> 10
 ccaggtaccg ttggtgctgt ttaagaccg 29

<210> 11
 <211> 760
 <212> PRT
 <213> Drosophila melanogaster

<400> 11

Met Asn Ser Thr Lys Val Pro Pro Glu Trp Lys Arg Arg Val Lys Ser
1 5 10 15

Glu Tyr Ile Lys Ile Arg Gln Gln Lys Arg Tyr Lys Arg Ala Asp Glu
20 25 30

Ile Lys Glu Ala Trp Ile Arg Asn Trp Asp Glu His Asn His Asn Val
35 40 45

Gln Asp Leu Tyr Cys Glu Ser Lys Val Trp Gln Ala Lys Pro Tyr Asp
50 55 60

Pro Pro His Val Asp Cys Val Lys Arg Ala Glu Val Thr Ser Tyr Asn
65 70 75 80

Gly Ile Pro Ser Gly Pro Gln Lys Val Pro Ile Cys Asx Ile Asn Ala
85 90 95

Val Thr Pro Ile Pro Thr Met Tyr Thr Trp Ala Pro Thr Gln Gln Asn
100 105 110

Phe Met Val Glu Asp Glu Thr Val Leu His Asn Ile Pro Tyr Met Gly
115 120 125

Asp Glu Val Leu Asp Lys Asp Gly Lys Phe Ile Glu Glu Leu Ile Lys
130 135 140

Asn Tyr Asp Gly Lys Val His Gly Asp Lys Asp Pro Ser Phe Met Asp
145 150 155 160

Asp Ala Ile Phe Val Glu Leu Val His Ala Leu Met Arg Ser Tyr Ser
165 170 175

Lys Glu Leu Glu Glu Ala Ala Pro Ser Thr Ser Thr Ala Ile Lys Thr
180 185 190

Glu Pro Leu Ala Lys Ser Lys Gln Gly Glu Asp Asp Gly Val Val Asp
195 200 205

Val Asp Ala Asp Cys Glu Ser Pro Met Lys Leu Glu Lys Thr Glu Ser
210 215 220

Lys Gly Asp Leu Thr Asp Val Glu Lys Lys Glu Thr Glu Glu Pro Val
225 230 235 240

Glu Thr Glu Asp Ala Asp Val Lys Pro Ala Val Glu Glu Val Lys Asp
245 250 255

Lys Leu Pro Phe Pro Ala Pro Ile Ile Phe Gln Ala Ile Ser Ala Asn
260 265 270

Phe Pro Asp Lys Gly Thr Ala Gln Glu Leu Lys Glu Lys Tyr Ile Glu
275 280 285

Leu Thr Glu His Gln Asp Pro Glu Arg Pro Gln Glu Cys Thr Pro Asn
290 295 300

Ile Asp Gly Ile Lys Ala Glu Ser Val Ser Arg Glu Arg Thr Met His
305 310 315 320

Ser Phe His Thr Leu Pro Cys Arg Arg Cys Phe Lys Tyr Asp Cys Phe
325 330 335

Leu His Arg Leu Gln Gly His Ala Gly Pro Asn Leu Gln Lys Arg Arg
340 345 350

Tyr Pro Glu Leu Lys Pro Phe Ala Glu Pro Cys Ser Asn Ser Cys Tyr
355 360 365

Met Leu Ile Asp Gly Met Lys Glu Lys Leu Ala Ala Asp Ser Lys Thr
370 375 380

Pro Pro Ile Asp Ser Cys Asn Glu Ala Ser Ser Glu Asp Ser Asn Asp
385 390 395 400

Ser Asn Ser Gln Phe Ser Asn Lys Asp Phe Asn His Glu Asn Ser Lys
405 410 415

Asp Asn Gly Leu Thr Val Asn Ser Ala Ala Val Ala Glu Ile Asn Ser
420 425 430

Ile Met Ala Gly Met Met Asn Ile Thr Ser Thr Gln Cys Val Trp Thr
435 440 445

Gly Ala Asp Gln Ala Leu Tyr Arg Val Leu His Lys Val Tyr Leu Lys
450 455 460

Asn Tyr Cys Ala Ile Ala His Asn Met Leu Thr Lys Thr Cys Arg Gln
465 470 475 480

Val Tyr Glu Phe Ala Gln Lys Glu Asp Ala Glu Ser Phe Ser Glu Asp
485 490 495

Leu Arg Gln Asp Phe Thr Pro Pro Arg Lys Lys Lys Lys Lys Gln Arg

500					505					510					
Leu	Trp	Ser	Leu	His	Cys	Arg	Lys	Ile	Gln	Leu	Lys	Lys	Asp	Ser	Ser
		515					520					525			
Ser	Asn	His	Val	Tyr	Asn	Tyr	Thr	Arg	Cys	Asp	His	Pro	Gly	His	Pro
	530					535					540				
Cys	Asp	Met	Asn	Cys	Ser	Cys	Ile	Gln	Thr	Gln	Asn	Phe	Cys	Glu	Lys
545					550					555					560
Phe	Cys	Asn	Cys	Ser	Ser	Asp	Cys	Gln	Asn	Arg	Phe	Pro	Gly	Cys	Arg
				565					570					575	
Cys	Lys	Ala	Gln	Cys	Asn	Thr	Lys	Gln	Cys	Pro	Cys	Tyr	Leu	Ala	Val
			580					585					590		
Arg	Glu	Cys	Asp	Pro	Asp	Leu	Cys	Gln	Ala	Cys	Gly	Ala	Asp	Gln	Phe
		595					600					605			
Lys	Leu	Thr	Lys	Ile	Thr	Cys	Lys	Asn	Val	Cys	Val	Gln	Arg	Gly	Leu
	610					615					620				
His	Lys	His	Leu	Leu	Met	Ala	Pro	Ser	Asp	Ile	Ala	Gly	Trp	Gly	Ile
625						630					635				640
Phe	Leu	Lys	Glu	Gly	Ala	Gln	Lys	Asn	Glu	Phe	Ile	Ser	Glu	Tyr	Cys
				645					650					655	
Gly	Glu	Ile	Ile	Ser	Gln	Asp	Glu	Ala	Asp	Arg	Arg	Gly	Lys	Val	Tyr
			660					665					670		
Asp	Lys	Tyr	Met	Cys	Ser	Phe	Leu	Phe	Asn	Leu	Asn	Asn	Asp	Phe	Val
		675					680					685			
Val	Asp	Ala	Thr	Arg	Lys	Gly	Asn	Lys	Ile	Arg	Phe	Ala	Asn	His	Ser
	690					695					700				
Ile	Asn	Pro	Asn	Cys	Tyr	Ala	Lys	Val	Met	Met	Val	Thr	Gly	Asp	His
705						710					715				720
Arg	Ile	Gly	Ile	Phe	Ala	Lys	Arg	Ala	Ile	Gln	Pro	Gly	Glu	Glu	Leu
				725					730					735	
Phe	Phe	Asp	Tyr	Arg	Tyr	Gly	Pro	Thr	Glu	Gln	Leu	Lys	Phe	Val	Gly
			740				745						750		

Ile Glu Arg Glu Met Glu Ile Val
755 760

<210> 12
<211> 134
<212> PRT
<213> Homo sapiens

<400> 12

Ser Pro Ile His Gly Arg Gly Leu Phe Cys Lys Arg Asn Ile Asp Ala
1 5 10 15

Gly Glu Met Val Ile Glu Tyr Ala Gly Asn Val Ile Arg Ser Ile Gln
20 25 30

Thr Asp Lys Arg Glu Lys Tyr Tyr Asp Ser Lys Gly Ile Gly Cys Tyr
35 40 45

Met Phe Arg Ile Asp Asp Ser Glu Val Val Asp Ala Thr Met His Gly
50 55 60

Asn Arg Ala Arg Phe Ile Asn His Ser Cys Glu Pro Asn Cys Tyr Ser
65 70 75 80

Arg Val Ile Asn Ile Asp Gly Gln Lys His Ile Val Ile Phe Ala Met
85 90 95

Arg Lys Ile Tyr Arg Gly Glu Glu Leu Thr Tyr Asp Tyr Lys Phe Pro
100 105 110

Ile Glu Asp Ala Ser Asn Lys Leu Pro Cys Asn Cys Gly Ala Lys Lys
115 120 125

Cys Arg Lys Phe Leu Asn
130

<210> 13
<211> 132
<212> PRT
<213> Drosophila melanogaster

<400> 13

Ser His Ile His Gly Arg Gly Leu Tyr Cys Thr Lys Asp Ile Glu Ala
1 5 10 15

Gly Glu Met Val Ile Glu Tyr Ala Gly Glu Leu Ile Arg Ser Thr Leu
20 25 30

Thr Asp Lys Arg Glu Arg Tyr Tyr Asp Ser Arg Gly Ile Gly Cys Tyr
35 40 45

Met Phe Lys Ile Asp Asp Asn Leu Val Val Asp Ala Thr Met Arg Gly
50 55 60

Asn Ala Ala Arg Phe Ile Asn His Cys Cys Glu Pro Asn Cys Tyr Ser
65 70 75 80

Lys Val Val Asp Ile Leu Gly His Lys His Ile Ile Ile Phe Ala Val
85 90 95

Arg Arg Ile Val Gln Gly Glu Glu Leu Thr Tyr Asp Tyr Lys Phe Pro
100 105 110

Phe Glu Asp Glu Lys Ile Pro Cys Ser Cys Gly Ser Lys Arg Cys Arg
115 120 125

Lys Tyr Leu Asn
130

<210> 14
<211> 133
<212> PRT
<213> Caenorhabditis elegans

<400> 14

Ser Arg Ile His Gly Trp Gly Leu Tyr Ala Met Glu Ser Ile Ala Pro
1 5 10 15

Asp Glu Met Ile Val Glu Tyr Ile Gly Gln Thr Ile Arg Ser Leu Val
20 25 30

Ala Glu Glu Arg Glu Lys Ala Tyr Glu Arg Arg Gly Ile Gly Ser Ser
35 40 45

Tyr Leu Phe Arg Ile Asp Leu His His Val Ile Asp Ala Thr Lys Arg
50 55 60

Gly Asn Phe Ala Arg Phe Ile Asn His Ser Cys Gln Pro Asn Cys Tyr
65 70 75 80

Ala Lys Val Leu Thr Ile Glu Gly Glu Lys Arg Ile Val Ile Tyr Ser
85 90 95

Arg Thr Ile Ile Lys Lys Gly Glu Glu Ile Thr Tyr Asp Tyr Lys Phe
100 105 110

Pro Ile Glu Asp Asp Lys Ile Asp Cys Leu Cys Gly Ala Lys Thr Cys
115 120 125

Arg Gly Tyr Leu Asn
130

<210> 15
<211> 136
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 15

Ser Ala Ile His Asn Trp Gly Leu Tyr Ala Leu Asp Ser Ile Ala Ala
1 5 10 15

Lys Glu Met Ile Ile Glu Tyr Val Gly Glu Arg Ile Arg Gln Pro Val
20 25 30

Ala Glu Met Arg Glu Lys Arg Tyr Leu Lys Asn Gly Ile Gly Ser Ser
35 40 45

Tyr Leu Phe Arg Val Asp Glu Asn Thr Val Ile Asp Ala Thr Lys Lys
50 55 60

Gly Gly Ile Ala Arg Phe Ile Asn His Cys Cys Asp Pro Asn Cys Thr
65 70 75 80

Ala Lys Ile Ile Lys Val Gly Gly Arg Arg Arg Ile Val Ile Tyr Ala
85 90 95

Leu Arg Asp Ile Ala Ala Ser Glu Glu Leu Thr Tyr Asp Tyr Lys Phe
100 105 110

Glu Arg Glu Lys Asp Asp Glu Glu Arg Leu Pro Cys Leu Cys Gly Ala
115 120 125

Pro Asn Cys Lys Gly Phe Leu Asn
130 135

<210> 16
<211> 429
<212> PRT
<213> *Drosophila melanogaster*

<400> 16

Met Gly Val Ile Ala Lys Arg Pro Pro Lys Gly Glu Tyr Val Val Glu
1 5 10 15

Arg Ile Glu Cys Val Glu Asn Asp Gln Tyr Gln Pro Val Phe Phe Val
20 25 30

Lys Trp Leu Gly Tyr His Asp Ser Glu Asn Thr Trp Glu Ser Leu Ala
35 40 45

Asn Val Ala Asp Cys Ala Glu Met Glu Lys Phe Val Glu Arg His Gln
50 55 60

Gln Leu Tyr Glu Thr Tyr Ile Ala Lys Ile Thr Thr Glu Leu Glu Lys
65 70 75 80

Gln Leu Glu Ala Leu Pro Leu Met Glu Asn Ile Thr Val Ala Glu Val
85 90 95

Asp Ala Tyr Glu Pro Leu Asn Leu Gln Ile Asp Leu Ile Leu Leu Ala
100 105 110

Gln Tyr Arg Ala Ala Gly Ser Arg Ser Gln Arg Glu Pro Gln Lys Ile
115 120 125

Gly Glu Arg Ala Leu Lys Ser Met Gln Ile Lys Arg Ala Gln Phe Val
130 135 140

Arg Arg Lys Gln Leu Ala Asp Leu Ala Leu Phe Glu Lys Arg Met Asn
145 150 155 160

His Val Glu Lys Pro Ser Pro Pro Ile Arg Val Glu Asn Asn Ile Asp
165 170 175

Leu Asp Thr Ile Asp Ser Asn Phe Met Tyr Ile His Asp Asn Ile Ile
180 185 190

Gly Lys Asp Val Pro Lys Pro Glu Ala Gly Ile Val Gly Cys Lys Cys
195 200 205

Thr Glu Asp Thr Glu Glu Cys Thr Ala Ser Thr Lys Cys Cys Ala Arg
210 215 220

Phe Ala Gly Glu Leu Phe Ala Tyr Glu Arg Ser Thr Arg Arg Leu Arg
225 230 235 240

Leu Arg Pro Gly Ser Ala Ile Tyr Glu Cys Asn Ser Arg Cys Ser Cys
245 250 255

Asp Ser Ser Cys Ser Asn Arg Leu Val Gln His Gly Arg Gln Val Pro
260 265 270

Leu Val Leu Phe Lys Thr Ala Asn Gly Ser Gly Trp Gly Val Arg Ala
275 280 285

Ala Thr Ala Leu Arg Lys Gly Glu Phe Val Cys Glu Tyr Ile Glu Glu
290 295 300

Ile Ile Thr Ser Asp Glu Ala Asn Glu Arg Gly Lys Ala Tyr Asp Asp
305 310 315 320

Asn Gly Arg Thr Tyr Leu Phe Asp Leu Asp Tyr Asn Thr Ala Gln Asp
325 330 335

Ser Glu Tyr Thr Ile Asp Ala Ala Asn Tyr Gly Asn Ile Ser His Phe
340 345 350

Ile Asn His Ser Cys Asp Pro Asn Leu Ala Val Phe Pro Cys Trp Ile
355 360 365

Glu His Leu Asn Val Ala Leu Pro His Leu Val Phe Phe Thr Leu Arg
370 375 380

Pro Ile Lys Ala Gly Glu Glu Leu Ser Phe Asp Tyr Ile Arg Ala Asp
385 390 395 400

Asn Glu Asp Val Pro Tyr Glu Asn Leu Ser Thr Ala Val Arg Val Glu
405 410 415

Cys Arg Cys Gly Arg Asp Asn Cys Arg Lys Val Leu Phe
420 425

<210> 17
<211> 166
<212> PRT
<213> Homo sapiens

<400> 17

Thr Ala Lys Met Gly Trp Gly Val Arg Ala Leu Gln Thr Ile Pro Gln
1 5 10 15

Gly Thr Phe Ile Cys Glu Tyr Val Gly Glu Leu Ile Ser Asp Ala Glu
20 25 30

Ala Asp Val Arg Glu Asp Asp Ser Tyr Leu Phe Asp Leu Asp Asn Lys
35 40 45

Asp Gly Glu Val Tyr Cys Ile Asp Ala Arg Tyr Tyr Gly Asn Ile Ser
50 55 60

Arg Phe Ile Asn His Leu Cys Asp Pro Asn Ile Ile Pro Val Arg Val
65 70 75 80

Phe Met Leu His Gln Asp Leu Arg Phe Pro Arg Ile Ala Phe Phe Ser
85 90 95

Ser Arg Asp Ile Arg Thr Gly Glu Glu Leu Gly Phe Asp Tyr Gly Asp
100 105 110

Arg Phe Trp Asp Ile Lys Ser Lys Tyr Phe Thr Cys Gln Cys Gly Ser
115 120 125

Glu Lys Cys Lys His Ser Ala Glu Ala Ile Ala Leu Glu Gln Ser Arg
130 135 140

Leu Ala Arg Leu Asp Pro His Pro Glu Leu Leu Pro Glu Leu Gly Ser
145 150 155 160

Leu Pro Pro Val Asn Thr
165

<210> 18
<211> 139
<212> PRT
<213> Homo sapiens

<400> 18

Thr Gln Asn Lys Gly Trp Gly Ile Arg Cys Leu Asp Asp Ile Ala Lys
1 5 10 15

Gly Ser Phe Val Cys Ile Tyr Ala Gly Lys Ile Leu Thr Asp Asp Phe
20 25 30

Ala Asp Lys Glu Gly Leu Glu Met Gly Asp Glu Tyr Phe Ala Asn Leu
35 40 45

Asp His Ile Glu Ser Val Glu Tyr Ile Ile Asp Ala Lys Leu Glu Gly
50 55 60

Asn Leu Gly Arg Tyr Leu Asn His Ser Cys Ser Pro Asn Leu Phe Val
65 70 75 80

Gln Asn Val Phe Val Asp Thr His Asp Leu Arg Phe Pro Trp Val Ala
85 90 95

Phe Phe Ala Ser Lys Arg Ile Arg Ala Gly Thr Glu Leu Thr Trp Asp
100 105 110

Tyr Asn Tyr Glu Val Gly Ser Val Glu Gly Lys Glu Leu Leu Cys Cys
115 120 125

Cys Gly Ala Ile Glu Cys Arg Gly Arg Leu Leu
130 135

<210> 19
<211> 20
<212> PRT
<213> Homo sapiens

<400> 19

Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala Pro
1 5 10 15

Arg Lys Gln Leu
20

<210> 20
<211> 20
<212> PRT
<213> Homo sapiens

<400> 20

Met Gly Pro Arg Arg Arg Ser Arg Lys Pro Glu Ala Pro Arg Arg Arg
1 5 10 15

Ser Pro Ser Pro
20

<210> 21
<211> 20
<212> PRT
<213> Rattus sp.

<400> 21

Met Ser Ser Arg Gly Gly Lys Lys Lys Ser Thr Lys Thr Ser Arg Ser
1 5 10 15

Ala Lys Ala Gly
20